In the Specification

Please amend the paragraph bridging page 5, lines 34 to page 6, line 10 to read as follows:

"By "hairless protein (HR)" is meant herein the mouse hairless protein. By "truncated hairless protein (HRt)" is meant the sequence provided as SEQ ID NO [[18]]17, which is amino acid residues 490-1182 of the C-terminal portion of mouse HR protein. Derivatives, fragments, or analogs of HR known to one of skill in the art in light of the present disclosure are considered equivalents of HR. It should be noted and underscored that mouse HR is greater than 80% identical to human HR. Thus, the interacting partners provided herein are expected to interact with human hairless protein in the same manner as such interacting partners interact within mouse HR. Accordingly, an antagonist and/or agonist compound having activity for HRt is expected to further exhibit activity for HR. Antagonists or agonists of the present HRt-IP complexes are further expected to exhibit activity for human hairless protein interacting partner equivalents.

Please amend the paragraph on page 7, lines 7-28 to read as follows:

"In the context of the present invention, the "bait" protein is a C-terminal portion of hairless protein of mouse (HRt) having amino acid residues 490 to 1182 (provided as SEQ ID NO:17)[[,]]; the nucleic acid sequence encoding amino acids 490 to 1182 is provided as SEQ ID NO:18) "Structure and Expression of the Hairless Gene of Mice," Begona, M., *et al.*, *J. Proc. Natl. Acad. Sci, USA* 91:7717-7721, 1994) (GenBank accession no. Z32675). HR protein (aa residues 490 to 1182) contains the zinc finger domain (595-620) and three PEST domains previously identified to be potentially important for HR function. To reiterate, mouse HR very similar to human HR. Indeed, PEST sequences are often used to serve as signals for rapid protein degradation. The signals may be constitutive or conditional. The PEST-FIND computer program has been developed by M. Rechsteiner and S. W. Rogers (*PEST sequences andregulation by proteolysis, TIBS 21, July 1996*) to objectively determine whether a protein contains a PEST region. The associated algorithm, available in PC/GENE (OMIGA), defines a

PEST sequence as a hydrophilic stretch of 12 or more aa residues containing at least one of each of P, E/D, and S/T in any order. PEST sequences must further be flanked by basic aa residues K, A or H, but basic residues are disallowed in the PEST sequence. PEST-FIND produces a score ranging from about +50 to –50. For classification purposes, a score of less than zero denotes a possible PEST region, but a score of greater than +5 denotes a high potential of the existence of a PEST region. For example, PEST Domains were located in the following regions of the HR protein (aa residues 490 to 1182): PEST Domain 12.26 between aa residues 522 and 546; PEST Domain 7.56 between aa residues 709 and 722; and PEST Domain 21.71 between aa residues 729 and 744."

Please amend the paragraph bridging page 27, line 29 to page 28, line 21 to read as follows:

Cloning and characterization of mouse Hairless (HR) cDNA

Oligonucleotides are designed to PCR-amplify the desired portion of mouse HR cDNA, based on the published sequence for mouse HR "Structure and Expression of the Hairless Gene of Mice," Begona, M., *et al.*, *J. Proc. Natl. Acad. Sci*, USA 91: 7717-7721, 1994) (GenBank accession no. Z32675). The oligonucleotides are also designed to contain restriction enzyme recognition sites for *Eco* RI, *Xba* I, *Not* I and *Bam* HI restriction enzymes for subsequent manipulation of the PCR product. In particular, the restriction enzyme sites for *Eco* RI and *Not* I (noted as underlined and italicized in the oligonucleotides shown below) are particularly useful for subsequent cloning and manipulation. The forward and reverse oligonucleotide primer pairs 5'-CCG GAA TTC GTC ACC CAG TGC CAA AGC TGT (SEQ ID NO: 19) and 5'-CGG GAT CCT CTA GA*G CGG CCG CTT* ATT ATT TAG CTT CCT GTA ACG CCCC (SEQ ID NO: 20) are used to PCR amplify HR cDNA corresponding to nucleotides 1845-3923 of HR from mouse early anagen cDNA library. PCR amplification is performed using the standard PCR protocol supplied with the Advantage 2 PCR kit. The PCR product is analyzed by agarose gel electrophoresis and is found to have the expected size (approximately 2 Kb). The PCR product is excised with *Eco* RI and *Not* I restriction enzymes. The restricted product is gel-purified and inserted into *Eco* RI and *Not* I sites of pET32a, such that the insert makes an in-frame fusion

with upstream sequences. The resulting plasmid is designated pET32a-HRt. This plasmid is used for both nucleotide sequence confirmation as well as for protein expression in *E. coli*. The nucleotide sequence reveals changes at three positions (nucleotide position [[321]]2165, change from C to T causing a codon change from AGC to AGT; nucleotide position [[756]]2600, change from C to T causing a codon change from GAC to GAT; nucleotide position [[1076]]2915, change from T to C causing a codon change from CCT to CCC) from the published sequence (SEQ ID NO: [[17]]18). Amino acid number 1 of SEQ ID NO:[[18]]17 corresponds to amino acid residue 490 of the C-terminal portion of HR protein. This truncated HR(HRt) cDNA corresponds to amino acid residues 490-1182 of the C-terminal portion of HR protein.